

1 CCAACTGCAC CTCGGTCTTA TCGATTGAAT TCCCCGGGGA TCCTCTAGAG ATCCCTCGAC
61 CTGACCCAC GCGTCCGGAA CCTTTCACG CCGACAACT ACGGGGACGA TTTCTGATG
121 ATTTTTCGGG CTTTCGATCC ACCCTCTCC CTTCTCATGG GACTTGGGG ACAAGCGTC
1 M G L N G O S V
181 CCGACCCCT CAGCGCTCG AGCAGCGCG TATCCAGGAG CCAAGGACAG CTCGGGAACC
9 P T A S S A R A G R Y P G A R T A S G T
241 AGACCATGCC TCCTGGACCC CAGATCCTT AAGTTCGTC TCTTCATCT CCGGTTCTG
29 R P N L L D P K I L K F V V F I V A V L
301 CTGCGGTCG GGGTGAATC TGCCACCATC CCGCGGACG ACGAAGTTC CCAGCAGACA
49 L P V R V D E A T I P R Q D E V P Q Q T
361 GTGCCCCAC AGCAACAGAG GCGACGCTC AAGGAGGAG AGTGTCCAGC AGGATCTCAT
69 V A P Q Q Q R R S L K E E E C P A G S H
421 AGATCAGAT ATACTGAGC CTGTAAACCG TCACAGAGG GTGTGGATTA CACCATCTCT
89 R S E Y T G A C N P C T E G V D Y T I A
481 TCCACAAAT TGCCTCTTG CCTGCTATG ACAGTTTGA AATCAGGTCA AACAAATAA
109 S M N L P S C L L C T V C K S G Q T H K
541 AGTTCCTGA CCAGACCCAG AGACCCGTC TGTAGTGTG AAAAAGGAG CTTCCAGGAT
129 S S C T T T R D T V C Q C E K G S F Q D
601 AAAAATCCC CTGAGATGTG CCGAGCTGT AGAACAGGT GTCCAGAGAG GATGTCAGG
149 K H S P E M C R T C R T C P R G M V K
661 GTCAATAAT GTACGCCCCG GAGTGACATC AAGTCAAAA ATGAATCAGC TGCCAGTTC
169 V S H C T P R S D I K C K N E S A A S S
721 ACTGGGAAA CCCCAGCAGC GAGGAGACA GTGACACCA TCCTGGGAT GCTTCCCTCT
189 T G K T F A A E E T V T T I L G M L A S
781 CCTATCATC ACCTATCAT CATAGTGGT TTAGTCATCA TTTAGTGTG GGTGTGGT
209 P Y H Y L I I X V V L V I I L A V V V V
841 GCTTTTCAT GTCGAAGAA ATTCATTCT TACCTCAAG GCATCTGTC AAGTGTGGA
229 Q F S C R K K F I S Y L K G I C S G G G
901 GAGGTCCCG AAGGTGTGA CAGAGTCTT TTCCGGGCG GTTCATGTCC TTCACGATT
249 G G P E R V H R V L F R R R S C P S R V
961 CTTGGGCGG AGGCAATGC CCGCAACGAG ACCTGAGTA ACAGATATT GCGACCCACC
269 P G A E D N A R N E T L S M R Y L Q P T
1021 CAGGTCTCTG AGCAGGAAT CCAAGGTCAG GAGCTGCGAG AGCTAACCGG TGTGACTGA
289 Q V S E Q E I Q G Q E L A E L T G V T V
1081 GAGT/GCCAG AGGAGCCACA GGTCTCTGT GACAGGACG AAGCTGAAGG GTGTGAGAG
309 E X₂₄ P E E P Q R L L E Q A E A E G C Q R
1141 AGGAGGCTGC TGGTCCAGT GATGACGCT GACTCGGCTG ACATCAGCAC CTTGCTGGAT
329 R R L L V P V N D A D S A D I S T L L D
1201 GCTCGGCAA CACTGGAAGA AGGACATGA AAGGAACAA TTCAGGACCA ACTGCTGGC
349 A S A T L E E G H A K E T I Q D Q L V G
1261 TCCGAAAGC TCTTTTATGA AGAGATGAG GCAAGCTCTG CTACGCTGT CTTGTGAAG
369 S E K L F Y E E D E A G S A T S C L
1321 AATCTCTCA GGAACCCAGA GCTTCCCTCA TTTACCTTTT CTCTACAAA GCGAGCAGC
1381 CTGAGAGAAA CAGTCCAGTA CTTGACCCAT GCGCCACAA ACTCTACTAT CCAATATGG
1441 GCACTTACC AATGTCCTA GAACTTGTG AACGCACTG GAGTAATTTT TATGAATAC
1501 TCGGTGTGAT AAGCAACCG GAGAAATTA TATCAGATC TTGCTGCTAT AGTTATACGA
1561 TTGTGTATTA AGGTCGTTT TAGGCCCAT GCGGTGCTC ATGCTGTAA TCCAGCACT
1621 TTGATAGCT GAGCCAGGTG GATTGCTGA GCTCGGAGT TTGAGACCG CTTATCAAC
1681 ACAGTGAAC TCCATCTCAA TTTAAAAAGA AAAAAGTGG TTTAGGATG TCATTCTTG
1741 CAGTCTTCA TCATGAGACA AGTCTTTTT TCTCTCTCT ATATTGCAAG CTCATCTCT
1801 ACTGCTGTG GCATTTAATG ACATCTAAT ACAGATGCG CACAGCCACA ATGCTTTGCC
1861 TTATATTTT TTAATTTAG AACGGGATTA TCTGTGAT ACCTGTATT TCAGTTTCG
1921 ATATTTTGA CTTATGATG AGATTATCA GACGTACCC TATGCTAAT CATGAGATA
1981 TGACTTACG AGGTTCCAG TTAGATTTT GAGCTTAAG ATAGATTAT TGGGGCTTA
2041 CCCCCACCTT AATTAGAAGA AACATTTTAT ATTGCTTTAC TA

Fig. 1A

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RTD 1 --MGLWGQSVPTASSARA--GRYPGARTASGTRPWLLDPKILKFVVFIVA
DR4 51 GRGALPTSMGQHGPSARARAGRAPGPRPAREASPRLRVHKTFKFV--VVG
DR5 1 --MEQRGQNAPAASGARKRHG--PGPREARGARGLRVPKTLVLV--VVA
DcR1 1 -----MARIPKTLKFVVVIVA

RTD 47 VLLPVRVDSATIPRQDEVPOQTVAPOQQRSLKEEECPAGSHRSEYTGAC
DR4 99 VLLQVVPSSAATIKLH---DQSIGTQQWEHSPLGELCPPGSHRSEYTGAC
DR5 45 VLLLVSALITQODLAPQORAAPQQRSSPSEGLCPPGHHISEDGRDC
DcR1 17 VLLPVLAISATTARQEEVPOQTVAPOQQRHSFKGEECPAGSHRSEYTGAC

CRD1

RTD 97 NPCTEGVDYTIASNNLPSCLLCTVCKSGQTNKSSCTTTRDTVCQCEKGSF
DR4 146 NRCTEGVGTYTNASNNLFACLPCTACKSDEEERSPCTTTRNTACQCKPGTF
DR5 95 ISCKYQDYSTHWNDLLFCLRCTRCDSEVELSPCTTTRNTVCQCEEGTF
DcR1 67 NPCTEGVDYTNASNNPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEG

CRD2

RTD 147 QDKNSPEHCRTCRGTGCPRGHVKVSNCPTPRSDIKCKNESAASSTGKTPAAE
DR4 196 RNDNSAEHCRKCRSTGCPRGHVKVKDCTPWSIDIECVHKESGNHNIW----
DR5 145 REEDSPEHCRKCRGTGCPRGHVKVGDCPTPWSIDIECVHKESGIIIGVTVAA-
DcR1 117 RNENSPEHCRKCSR-CPSGEVQVSNCPSWDDIQCVVEEFGANAT-----

Fig. 1B

RTD 233 RKKFISYLGKICSGGGGGPERVHRVLFRRRSCPSRVPGAEDNARNETLSN
DR4 269 -GGDPKCMDRVCFWRLG-----LLRGPGAEDNAHNEILSN
DR5 209 --KVLPLYLGKICSGGGGDPERVDR-----SSQRPGAEDNVLNEIVSI

RTD 283 RYLQPTQVSEQEIQGQELAEITGVTVESPEEPQRLLEQAEAEGCQRRRL
DR4 303 ADSLSTFVSEQQMESQEPADLTGVTVQSPGEAQCLLGPAEAEGSQRRRL
DR5 250 --LQPTQVPEQEMEVEQEPAEPTGVNMLSPGESEHLLLEPAEAERSQRRRL

RTD 333 VPVNDAD-----DD-----
DR4 353 VPANGADPTETLMLFFDKFANIVPFDSWDQLMRQLDLTKNEIDVVRAGTA
DR5 298 VPANEGDPTETLRQCFDDFADLVPFDSWEPLMRKLGLMDNEIKVAKAEAA

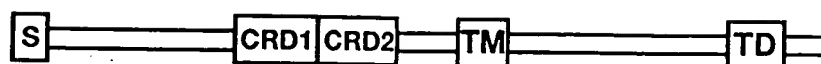
RTD 340 -----SADISTLLDASATLEEGMAKETIQDQLVGSE
DR4 403 GPGDALYAMLKWNKTGRNASIMTLLDALERMEERMAKEKIQDLLVDSG
DR5 348 GHRDTLYTMLIKWNKTGRDASVMTLLDALETGERLAKQKIEDHLLSSG

RTD 371 KLFYEDEEAGSATSCL
DR4 453 KFIYLEDGTGSAVSLE
DR5 398 KFMYLEGNADSALS

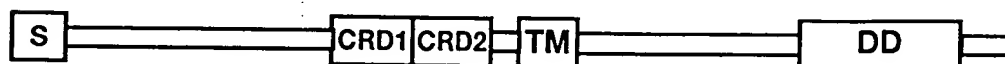
Fig. 1C

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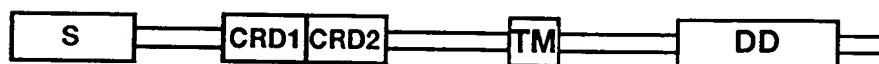
RTD



DR4



DR5



DcR1



Fig. 1D

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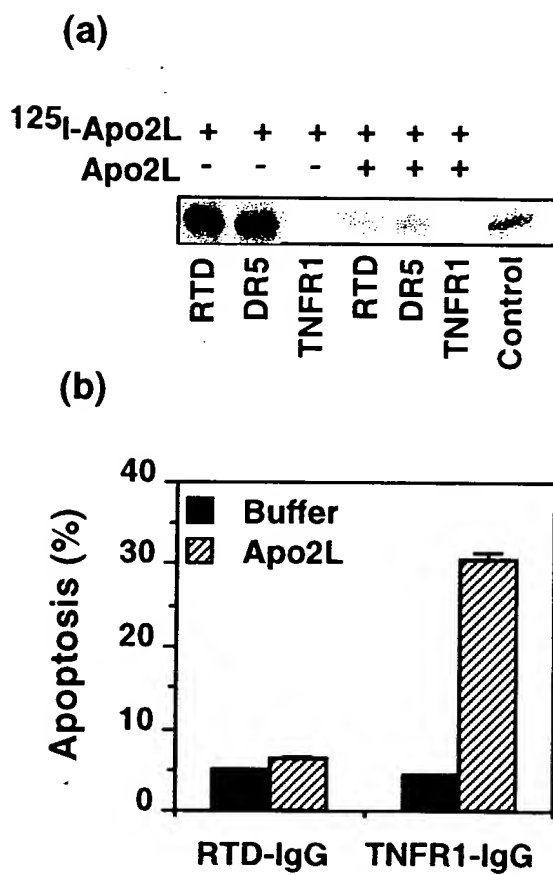


Fig. 2

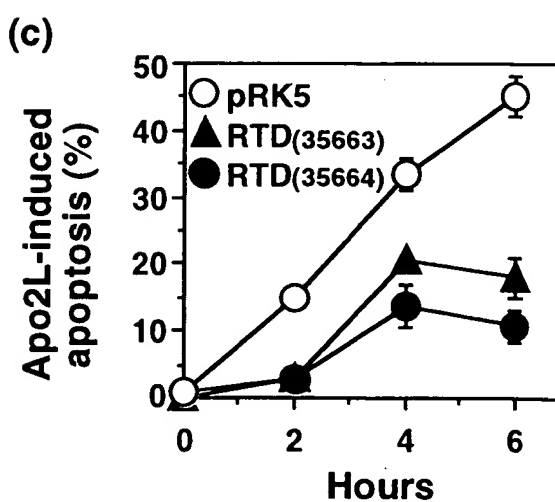
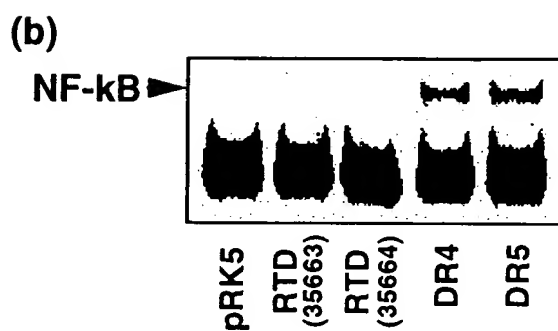
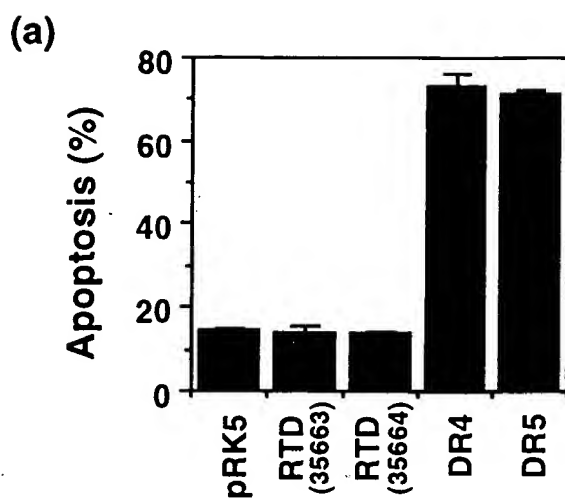


Fig. 3

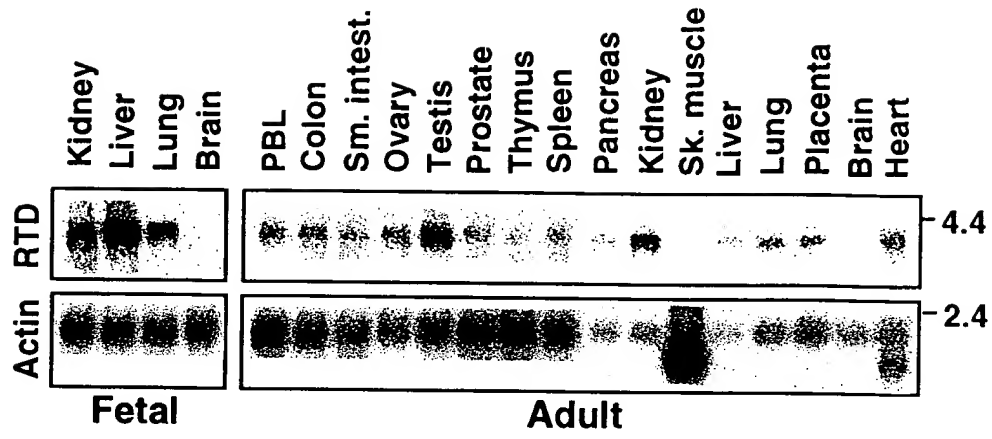


Fig. 4